

Complete Listing of Claims Pursuant to 37 C.F.R. §1.121

Pursuant to 37 C.F.R. §1.121 the following is a complete listing of the claims of the present application. In this set of claims, please amend the claims as follows. The following listing of claims will replace all prior versions of claims in the application:

1.-61. (canceled)

62. (currently amended) A G-CSF analog having hematopoietic activity comprising an internal core of helices A, B, C and D and external loops as set forth in FIG. 4 and an amino acid sequence, wherein the amino acid sequence differs from that of SEQ ID NO:2 in that

a) lysine residues at positions 17 and 41 are substituted; and

b) at least one amino acid sequence in an external loop is altered to include one or more lysine amino acid residues, wherein one or more of said lysine amino acid residues is covalently modified with polyethylene glycol (PEG); ~~and,~~

wherein[,] an N-terminal methionine as set forth in SEQ ID NO:2 is optional.

63.-65. (canceled)

66. (currently amended) A G-CSF analog having hematopoietic activity comprising an internal core of helices A, B, C and D and external loops as set forth in FIG. 4 and an amino acid sequence, wherein the amino acid sequence differs from that of SEQ ID NO:2 in that

a) lysine residues at positions 17 and 41 are substituted;

b) at least one amino acid sequence in an external loop is altered to include one or more lysine amino acid residues, wherein one or more of said lysine amino acid residues is covalently modified with polyethylene glycol (PEG); and

c) at least one amino acid residue in of helix A ~~amino acid sequence~~, other than at said lysine residue at position 17, one amino acid residue in helix C ~~amino acid sequence~~ and or one amino acid residue in helix D ~~amino acid sequence~~ is altered to include by substitution of one or more amino acid residues which are not essential for structural integrity,

and wherein[,] an N-terminal methionine as set forth in SEQ ID NO:2 is optional.

67.-74. (canceled)

75. (currently amended) A G-CSF analog having hematopoietic activity comprising an internal core of helices A, B, C and D and external loops as set forth in FIG. 4 and an amino acid sequence, wherein the amino acid sequence differs from that of SEQ ID NO:2 in that

a) lysine residues at positions 17 and 41 are substituted ~~with arginine~~; and

b) at least one ~~of helix A amino acid sequence, other than at said lysine residue at position 17, helix C amino acid sequence and helix D amino acid sequence~~ is altered to ~~include substitution of one or more amino acid residues~~ residue which ~~are~~ is not essential for structural integrity is substituted, said amino acid residue located in helix C or helix D;[,] and

c) at least one lysine amino acid residue is covalently modified with polyethylene glycol (PEG).

wherein[,] an N-terminal methionine as set forth in SEQ ID NO:2 is optional.

76. (currently amended) A G-CSF analog having hematopoietic activity comprising an internal core of helices A, B, C and D and external loops as set forth in FIG. 4 and an amino acid sequence, wherein the amino acid sequence differs from that of SEQ ID NO:2 in that

a) lysine residues at positions 17 and 41 are substituted ~~with arginine~~; and

b) ~~at least two of helix A amino acid sequence, amino acid residues, other than at said lysine residue at position 17 of helix A, helix C amino acid sequence and helix D amino acid sequence are altered to include substitution of one or more amino acid residues~~ which are not essential for structural integrity, are substituted, wherein the two substituted amino acid residues are located in different helices, said helices selected from the group consisting of helix A, helix C and helix D; and

c) at least one lysine amino acid residue is covalently modified with polyethylene glycol (PEG),

wherein[,] an N-terminal methionine as set forth in SEQ ID NO:2 is optional.

77. (canceled)

78. (canceled)

79. (currently amended) A G-CSF analog having hematopoietic activity comprising an internal core of helices A, B, C and D and external loops as set forth in FIG. 4 and an amino acid sequence, wherein the amino acid sequence differs from that of SEQ ID NO:2 in that

a) lysine residues at positions 17 and 41 are substituted; and

b) ~~at least three of helix A amino acid sequence, amino acid residues, other than at said lysine residue at position 17 of helix A, helix C amino acid sequence and helix D amino acid sequence are altered to include substitution of one or more amino acid residues~~ which are not essential for structural integrity, are substituted, wherein the three substituted amino acid residues are located in different helices, said helices selected from the group consisting of helix A, helix C and helix D; and

c) at least one lysine amino acid residue is covalently modified with polyethylene glycol (PEG),

wherein[,] an N-terminal methionine as set forth in SEQ ID NO:2 is optional.

80. (canceled)

81. (previously presented) The G-CSF analog of any one of claims 62, 66, 75-76, and 79, wherein the hematopoietic activity of said G-CSF analog *in vitro* is lower than the hematopoietic activity of unaltered recombinant human G-CSF *in vitro*.

82. (previously presented) The G-CSF analog of claim 81, wherein the serum half-life of the G-CSF analog is greater than the serum half-life of unaltered recombinant human G-CSF.

83. (previously presented) The analog of claim 81, wherein hematopoietic activity is determined by an *in vitro* tritiated thymidine assay.